

SEQUENCE LISTING

<110> DeBonte, Lorin R. Fan, Zhegong Miao, Guo-Hua <120> FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF <130> 07148-063003 <140> US 09/771,904 <141> 2001-01-29 <150> US 08/874,109 <151> 1997-06-12 <160> 70 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 1155 <212> DNA <213> Brassica napus <220> <221> CDS <222> (1)...(1152) <223> Wild type Fad2 <221> misc feature <222> 205 <223> n = a, g, c, or t/u<400> 1 atg ggt gca ggt gga aga atg caa gtg tct cct ccc tcc aag aag tct 48 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act 96 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr 20 25 gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg 144 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser 35 40 45 ate cet ege tet the tee tac etc ate tgg gae ate ate ata gee tee 192 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 50 55 60 tge tte tac tac nte gee ace act tac tte cet etc ect cac cet 240 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro

65					70				75					80	
						cct Pro			-	_			_	_	288
			-		-	ata Ile		-	_				-		336
_	_		_			gac Asp	_	_							384
			_			ttc Phe 135		 _		_		_	_		432
						ctc Leu									480
_	_		_		_	tgg Trp		 _						_	528
	_			_		acg Thr							-		576
		_			_	tcg Ser								_	624
_						gct Ala 215				_	_		_		672
_					_	gct Ala			-	-	_				720
	_		_	_		cag Gln		 _	_	_	_	_			768
	_	_		_		gtc Val					_				816
_	_		-			tcc Ser	_			_	_				864

Asp Trp Phe 2	agg gga g Arg Gly A								912
ttg aac aag o Leu Asn Lys v 305	Val Phe H								960
ccg ttc tcc a		_			_		_		1008
ata aag ccg a Ile Lys Pro									1056
gtt aag gcg a Val Lys Ala 1 355		rg Glu <i>F</i>							1104
gac agg caa (Asp Arg Gln (370									1152
tga									1155
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<212> PRT <213> Brassi	ca napus								
	-	Ile, o	r Val						
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<213> Brassi <220> <223> Xaa = <400> 2 Met Gly Ala 1 Glu Thr Asp Val Gly Glu 35 Ile Pro Arg 50 Cys Phe Tyr	Phe, Leu, Gly Gly A 5 Thr Ile I 20 Leu Lys I Ser Phe S	Arg Met O ys Arg V ys Ala I Ser Tyr I 55 Ala Thr I	Gln Val Val Pro 25 Ile Pro 40 Leu Ile	10 Cys Glu Pro His Trp Asp Phe Pro	Thr Pro Cys Phe 45 Ile Ile 60	Pro 30 Lys Ile	15 Phe Arg Ala	Thr Ser Ser Pro	
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His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
                    150
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
                165
                                    170
Gly Arq Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
                                185
                                                     190
            180
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
                            200
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
                        215
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
                    230
                                         235
Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
                                265
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
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                            280
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
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                                             300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
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                                         315
Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
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                325
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
            340
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Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
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                                             380
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gaa acc gac acc atc aag cgc gta ccc tgc gag aca ccg ccc ttc act
Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
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25

20

_		_		_	aaa Lys	-			_		-			_	_	3	144
		_			tcc Ser					_				_]	192
-					gcc Ala 70											2	240
				_	tgg Trp					_	_			_	_	2	288
			_		gtc Val		_		_	_				_		3	336
_	_		_		ctt Leu	_	_		_							3	384
			_		tac Tyr				_		_		_	_		4	432
					tcc Ser 150			_	_	-			-		_	4	480
_	_		_		aag Lys											į	528
					tta Leu											į	576
		_			gtc Val	_		_			_					(624
_					aac Asn	_						_		_		(672
_					gac Asp 230	_				_	_					•	720

ttc cgt tac gcc g Phe Arg Tyr Ala A 2				768
gga gtc ccg ctt c Gly Val Pro Leu L 260	-		_	816
ttg cag cac acg c Leu Gln His Thr H 275	_	Pro His Tyr Asp		864
gat tgg ttc agg g Asp Trp Phe Arg G 290			Asp Tyr Gly Ile	912
ttg aac aag gtc t Leu Asn Lys Val P 305				960
ccg ttc tcc acg a Pro Phe Ser Thr M 3	-			8000
ata aag ccg ata c Ile Lys Pro Ile I 340				1056
gtt aag gcg atg t Val Lys Ala Met T 355		Lys Glu Cys Ile		L104
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tga			1	L155
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Glu Thr Asp Thr I	Ile Lys Arg Val		Pro Pro Phe Thr	
Val Gly Glu Leu I 35	Lys Lys Ala Ile 40		Phe Lys Arg Ser 45	

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Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
                     70
                                         75
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
                85
Leu Thr Gly Val Trp Val Ile Ala His Lys Cys Gly His His Ala Phe
            100
                                105
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
                            120
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
                        135
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
                    150
                                        155
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
               165
                                   170
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
                               185
           180
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
                            200
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
                        215
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
                    230
                                        235
Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
                245
                                    250
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
                                265
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
                            280
Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
                        295
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
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Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
                325
                                    330
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
                                345
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
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Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
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<211> 1155

<212> DNA

<213> Brassica napus

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<222> (1)...(1152)

<223> Wild type Fad2

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		_				tac Tyr 55				_					192
_				_	_	acc Thr							_		240
				_		cct Pro				-	_	_	 _	_	288
			_		-	ata Ile	_			_					336
						gac Asp									384
			_			ttc Phe 135			_						432
						ctc Leu									480
						tgg Trp									528
	_			_		acg Thr	_	_							576
		_				tcg Ser									624

tgc cat ttc Cys His Phe 210		_			_	_		_	672
cag ata tac Gln Ile Tyr 225				Leu A	-	_			720
tac cgc tac Tyr Arg Tyr		_		_		_	_		768
gga gtt ccg Gly Val Pro	-								816
ttg cag cac Leu Gln His	Thr His		_		_	_			 864
gat tgg ttg Asp Trp Let 290		-							912
ttg aac aag Leu Asn Lys 305	_		_	Asp T	_				960
ctg ttc tcg Leu Phe Sei	_	_							1008
ata aag ccc Ile Lys Pro				Gln I					1056
gtt aag gcg Val Lys Ala 359	Met Trp				_				1104
gac agg caa Asp Arg Gli 370									1152
tga									1155
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                             40
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
                         55
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
                    70
                                        75
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
                            120
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
                                           140
                       135
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
                    150
                                        155
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
                165
                                    170
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
                                185
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
                            200
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
                        215
                                            220
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
                    230
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
                                   250
               245
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
                               265
            260
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
                            280
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
                        295
                                            300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
                    310
                                        315
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
                325
                                    330
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Leu His Gly Thr Pro Val
                                345
Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
                           360
Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
    370
                        375
                                            380
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<210> 7

<211> 1155

<212> DNA

<213> Brassica napus

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tac tta Tyr Leu	_	_	_		y Arg		_				_	624
tgc cat Cys His 210			Asn A				_	_	_	_		672
cag ata Gln Ile 225		Ser A	_									720
tac cgc Tyr Arg	_	_	_		_	-						768
gga gtt Gly Val	_	Leu :	_					_				816
ttg cag Leu Gln					u Pro		_	-				864
gat tgg Asp Trp 290			Ala L									912
ttg aac Leu Asn 305		Phe I										960
ctg ttc Leu Phe	_	_	_									1008
ata aag Ile Lys	_	e Leu (_		Gln						1056
gtt aag Val Lys					a Lys							1104
gac agg Asp Arg 370	Gln Gl		Lys L									1152
tga												1155

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<212> PRT

<213> Brassica napus

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<211> 1155 <212> DNA <213> Brassica napus <220> <221> CDS <222> (1) . . . (1152) <400> 9 atg ggt gca ggt gga aga atg caa gtg tct cct ccc tcc aaa aag tct 48 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser 10 gaa acc gac aac atc aag cgc gta ccc tgc gag aca ccg ccc ttc act 96 Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr gtc gga gaa ctc aag aaa gca atc cca ccg cac tgt ttc aaa cgc tcg 144 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser atc cct cgc tct ttc tcc tac ctc atc tgg gac atc atc ata gcc tcc 192 Ile Pro Arq Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser 55 50 tgc ttc tac tac gtc gcc acc act tac ttc cct ctc cct cac cct 240 Cys Phe Tyr Tyr Val Ala Thr Tyr Phe Pro Leu Leu Pro His Pro 65 75 288 ctc tcc tac ttc gcc tgg cct ctc tac tgg gcc tgc cag ggc tgc gtc Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val cta acc ggc gtc tgg gtc ata gcc cac gag tgc ggc cac cac gcc ttc 336 Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe 100 105 age gae tae cag tgg etg gae gae ace gte gge ete ate tte cae tee 384 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser 115 120 tte etc etc gte ect tae tte tec tgg aag tae agt eat ega ege eac 432 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His 130 135 cat tcc aac act ggc tcc ctc gag aga gac gaa gtg ttt gtc ccc aag 480 His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys 150 155 aag aag tca gac atc aag tgg tac ggc aag tac ctc aac aac cct ttg 528 Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu 165 170 175

	cgc Arg															576	
	tta Leu	-			_	_		_			-				_	624	
-	cat His 210					_					_	_		_		672	
	ata Ile															720	
	cgc Arg		_	_	_			-	-	_	_	_	_			768	
	gtt Val			_		_					_	_				816	
_	cag Gln		_				_									864	
	tgg Trp 290															912	
_	aac Asn	_	_					_	_	_						960	
_	ttc Phe	_		_	_											1008	
	aag Lys															1056	
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<213> Brassica napus
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Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
                             40
Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
                    70
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
               85
                                    90
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
            100
                                105
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
                            120
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
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                                            140
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
                    150
                                        155
Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
                                    170
Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
                               185
                                                    190
Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala
                            200
        195
Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
                        215
Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
                    230
                                        235
Tyr Arg Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Tyr
                                    250
                245
Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
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            260
Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
                            280
Asp Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
                        295
                                            300
Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
                    310
                                        315
Leu Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
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                                    330
Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
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Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
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	_		_	_	tta Leu								576
		-			gtc Val	_		_			-	_	624
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Cys	50 Phe	Tyr	Tyr	Val	Ala	55 Thr	Thr	Tyr	Phe			Leu	Pro	His		
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